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Reviewer: Durreshwar Anjum

Timestamp: Wed Sep 12 11:55:09 EDT 2007

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Application No: 10573969 Version No: 1.0

**Input Set:**

**Output Set:**

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**Total Warnings:** 0  
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**No. of SeqIDs Defined:** 7  
**Actual SeqID Count:** 7

## SEQUENCE LISTING

&lt;110&gt; SUGIURA, Takeyuki

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&lt;130&gt; Q94181

&lt;140&gt; 10573969

&lt;141&gt; 2007-08-31

&lt;150&gt; PCT/JP2004/014812

&lt;151&gt; 2004-09-30

&lt;150&gt; JP 2003-341245

&lt;151&gt; 2003-09-30

&lt;160&gt; 7

&lt;170&gt; PatentIn version 3.1

&lt;210&gt; 1

&lt;211&gt; 2934

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

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&lt;222&gt; (1)..(93)

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Gln Pro Pro Gly Pro Pro Arg Arg Leu Arg Val Pro Cys Arg Ala Ser  
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Ser Gly Gly Gly Gly Gly Gly Arg Glu Gly Leu Leu Gly  
35 40 45

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Gln Arg Arg Pro Gln Asp Gly Gln Ala Arg Ser Ser Cys Ser Pro Gly  
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Gly Arg Thr Pro Ala Ala Arg Asp Ser Ile Val Arg Glu Val Ile Gln  
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Lys Pro Val Leu Ala Ile Ile Gln Ala Gly Asp Asp Asn Leu Met Gln			
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gaa atc aac cag aat ttg gct gag gag gct ggt ctg aac atc act cac			384
Glu Ile Asn Gln Asn Leu Ala Glu Glu Ala Gly Leu Asn Ile Thr His			
115	120	125	
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Ile Cys Leu Pro Pro Asp Ser Ser Glu Ala Glu Ile Ile Asp Glu Ile			
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Leu Lys Ile Asn Glu Asp Thr Arg Val His Gly Leu Ala Leu Gln Ile			
145	150	155	160
tct gag aac ttg ttt agc aac aaa gtc ctc aat gcc ttg aaa cca gaa			528
Ser Glu Asn Leu Phe Ser Asn Lys Val Leu Asn Ala Leu Lys Pro Glu			
165	170	175	
aaa gat gtg gat gga gta aca gac ata aac ctg ggg aag ctg gtg cga			576
Lys Asp Val Asp Gly Val Thr Asp Ile Asn Leu Gly Lys Leu Val Arg			
180	185	190	
ggg gat gcc cat gaa tgt ttt gtt tca cct gtt gcc aaa gct gta att			624
Gly Asp Ala His Glu Cys Phe Val Ser Pro Val Ala Lys Ala Val Ile			
195	200	205	
gaa ctt ctt gaa aaa tca ggt gtc aac cta gat gga aag aag att ttg			672
Glu Leu Leu Glu Lys Ser Gly Val Asn Leu Asp Gly Lys Lys Ile Leu			
210	215	220	
gta gtg ggg gcc cat ggg tct ttg gaa gct gct cta caa tgc ctg ttc			720
Val Val Gly Ala His Gly Ser Leu Glu Ala Ala Leu Gln Cys Leu Phe			
225	230	235	240
cag aga aaa ggg tcc atg aca atg agc atc cag tgg aaa aca cgc cag			768
Gln Arg Lys Gly Ser Met Thr Met Ser Ile Gln Trp Lys Thr Arg Gln			
245	250	255	
ctt caa agc aag ctt cac gag gct gac att gtg gtc cta ggc tca cct			816
Leu Gln Ser Lys Leu His Glu Ala Asp Ile Val Val Leu Gly Ser Pro			
260	265	270	
aag cca gaa gag att ccc ctt act tgg ata caa cca gga act act gtt			864
Lys Pro Glu Glu Ile Pro Leu Thr Trp Ile Gln Pro Gly Thr Thr Val			
275	280	285	
ctc aac tgc tcc cat gac ttc ctg tca ggg aag gtt ggg tgt ggc tct			912
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ctt gct gca gct ctg cga att cag aac atg gtc agt agt gga agg aga				1008
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325		330		335
tgg ctt cgt gaa cag cag cac agg cgg tgg aga ctt cac tgc ttg aaa				1056
Trp	Leu	Arg	Glu	Gln Gln His Arg Arg Trp Arg Leu His Cys Leu Lys
340		345		350
ctt cag cct ctc tcc cct gtg cca agt gac att gag att tca aga gga				1104
Leu	Gln	Pro	Leu	Ser Pro Val Pro Ser Asp Ile Glu Ile Ser Arg Gly
355		360		365
caa act cca aaa gct gtg gat gtc ctt gcc aag gag att gga ttg ctt				1152
Gln	Thr	Pro	Lys	Ala Val Asp Val Leu Ala Lys Glu Ile Gly Leu Leu
370		375		380
gca gat gaa att gaa atc tat ggc aaa agc aaa gcc aaa gta cgt ttg				1200
Ala	Asp	Glu	Ile	Glu Ile Tyr Gly Lys Ser Ala Lys Val Arg Leu
385		390		395
tcc gtg cta gaa agg tta aag gat caa gca gat gga aaa tac gtc tta				1248
Ser	Val	Leu	Glu	Arg Leu Lys Asp Gln Ala Asp Gly Lys Tyr Val Leu
405		410		415
gtt gct ggg atc aca ccc acc cct ctt gga gaa ggg aag agc aca gtc				1296
Val	Ala	Gly	Ile	Thr Pro Thr Pro Leu Gly Glu Gly Lys Ser Thr Val
420		425		430
acc atc ggg ctt gtg cag gct ctg acc gca cac ctg aat gtc aac tcc				1344
Thr	Ile	Gly	Leu	Val Gln Ala Leu Thr Ala His Leu Asn Val Asn Ser
435		440		445
ttt gcc tgc ttg agg cag cct tcc caa gga ccg acg ttt gga gtg aaa				1392
Phe	Ala	Cys	Leu	Arg Gln Pro Ser Gln Gly Pro Thr Phe Gly Val Lys
450		455		460
gga gga gcc gcg ggt ggt gga tat gcc cag gtc atc ccc atg gag gag				1440
Gly	Gly	Ala	Ala	Gly Gly Tyr Ala Gln Val Ile Pro Met Glu Glu
465		470		475
ttc aac ctt cac ttg act gga gac atc cac gcc atc acc gct gcc aat				1488
Phe	Asn	Leu	His	Leu Thr Gly Asp Ile His Ala Ile Thr Ala Ala Asn
485		490		495
aac ttg ctg gct gcc gcc atc gac acg agg att ctt cat gaa aac acg				1536
Asn	Leu	Leu	Ala	Ala Ile Asp Thr Arg Ile Leu His Glu Asn Thr
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caa aca gat aag gct ctg tat aat cgg ctg gtt cct tta gtg aat ggt				1584
Gln	Thr	Asp	Lys	Ala Leu Tyr Asn Arg Leu Val Pro Leu Val Asn Gly
515		520		525
gtc aga gaa ttt tca gaa att cag ctt gct cgg cta aaa aaa ctg gga				1632
Val	Arg	Glu	Phe	Ser Glu Ile Gln Leu Ala Arg Leu Lys Lys Leu Gly
530		535		540

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ttg gat aca aat gac cga ttt cta cga aaa ata acc atc ggg cag gga Leu Asp Thr Asn Asp Arg Phe Leu Arg Lys Ile Thr Ile Gly Gln Gly 580	585	590		1776
aac aca gag aag ggc cat tac cgg cag gcg cag ttt gac atc gca gtg Asn Thr Glu Lys Gly His Tyr Arg Gln Ala Gln Phe Asp Ile Ala Val 595	600	605		1824
gcc agc gag atc atg gcg gtg ctg gcc ctg acg gac agc ctc gca gac Ala Ser Glu Ile Met Ala Val Leu Ala Leu Thr Asp Ser Leu Ala Asp 610	615	620		1872
atg aag gca cgg ctg gga agg atg gtg gtg gcc agt gac aaa agc ggg Met Lys Ala Arg Leu Gly Arg Met Val Val Ala Ser Asp Lys Ser Gly 625	630	635	640	1920
cag cct gtg aca gca gat gat ttg ggg gtg aca ggt gct ttg aca gtt Gln Pro Val Thr Ala Asp Asp Leu Gly Val Thr Gly Ala Leu Thr Val 645	650	655		1968
ttg atg aaa gat gca ata aaa cca aac ctg atg cag acc ctg gaa ggg Leu Met Lys Asp Ala Ile Lys Pro Asn Leu Met Gln Thr Leu Glu Gly 660	665	670		2016
aca cct gtg ttc gtg cat gcg ggc cct ttt gct aac att gct cac ggc Thr Pro Val Phe Val His Ala Gly Pro Phe Ala Asn Ile Ala His Gly 675	680	685		2064
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gag aaa ttc ttc aac atc aag tgc cga gct tcc ggc ttg gtg ccc aac Glu Lys Phe Phe Asn Ile Lys Cys Arg Ala Ser Gly Leu Val Pro Asn 725	730	735		2208
gtg gtt gtg tta gtg gca acg gtg cga gct ctg aag atg cat gga ggc Val Val Val Leu Val Ala Thr Val Arg Ala Leu Lys Met His Gly Gly 740	745	750		2256
ggg cca agt gta acg gct ggt gtt cct ctt aag aaa gaa tat aca gag Gly Pro Ser Val Thr Ala Gly Val Pro Leu Lys Lys Glu Tyr Thr Glu 755	760	765		2304

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770	775	780	
att cag atc act cag ctc ttt ggg gtt ccc gtt gtg gtg gct ctg aat			2400
Ile Gln Ile Thr Gln Leu Phe Gly Val Pro Val Val Val Ala Leu Asn			
785	790	795	800
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Val Phe Lys Thr Asp Thr Arg Ala Glu Ile Asp Leu Val Cys Glu Leu			
805	810	815	
gca aag cgg gct ggt gcc ttt gat gca gtc ccc tgc tat cac tgg tcg			2496
Ala Lys Arg Ala Gly Ala Phe Asp Ala Val Pro Cys Tyr His Trp Ser			
820	825	830	
gtt ggt gga aaa gga tcg gtg gac ttg gct cgg gct gtg aga gag gct			2544
Val Gly Gly Lys Gly Ser Val Asp Leu Ala Arg Ala Val Arg Glu Ala			
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gcg agt aaa aga agc cga ttc cag ttc ctg tat gat gtt cag gtt cca			2592
Ala Ser Lys Arg Ser Arg Phe Gln Phe Leu Tyr Asp Val Gln Val Pro			
850	855	860	
att gtg gac aag ata agg acc att gct cag gct gtc tat gga gcc aaa			2640
Ile Val Asp Lys Ile Arg Thr Ile Ala Gln Ala Val Tyr Gly Ala Lys			
865	870	875	880
gat att gaa ctc tct cct gag gca caa gcc aaa ata gat cgt tac act			2688
Asp Ile Glu Leu Ser Pro Glu Ala Gln Ala Lys Ile Asp Arg Tyr Thr			
885	890	895	
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Gln Gln Gly Phe Gly Asn Leu Pro Ile Cys Met Ala Lys Thr His Leu			
900	905	910	
tct cta tct cac caa cct gac aaa aaa ggt gtg cca agg gac ttc atc			2784
Ser Leu Ser His Gln Pro Asp Lys Lys Gly Val Pro Arg Asp Phe Ile			
915	920	925	
tta cct atc agt gac gtc cgg gcc agc ata ggc gct ggg ttc att tac			2832
Leu Pro Ile Ser Asp Val Arg Ala Ser Ile Gly Ala Gly Phe Ile Tyr			
930	935	940	
cct ttg gtc gga acg atg agc acc atg cca gga ctg ccc acc cgg ccc			2880
Pro Leu Val Gly Thr Met Ser Thr Met Pro Gly Leu Pro Thr Arg Pro			
945	950	955	960
tgc ttt tat gac ata gat ctt gat acc gaa aca gaa caa gtt aaa ggc			2928
Cys Phe Tyr Asp Ile Asp Leu Asp Thr Glu Thr Glu Gln Val Lys Gly			
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ttg ttc			2934
Leu Phe			

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35 40 45

Gln Arg Arg Pro Gln Asp Gly Gln Ala Arg Ser Ser Cys Ser Pro Gly  
50 55 60

Gly Arg Thr Pro Ala Ala Arg Asp Ser Ile Val Arg Glu Val Ile Gln  
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Asn Ser Lys Glu Val Leu Ser Leu Leu Gln Glu Lys Asn Pro Ala Phe  
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Lys Pro Val Leu Ala Ile Ile Gln Ala Gly Asp Asp Asn Leu Met Gln  
100 105 110

Glu Ile Asn Gln Asn Leu Ala Glu Glu Ala Gly Leu Asn Ile Thr His  
115 120 125

Ile Cys Leu Pro Pro Asp Ser Ser Glu Ala Glu Ile Ile Asp Glu Ile  
130 135 140

Leu Lys Ile Asn Glu Asp Thr Arg Val His Gly Leu Ala Leu Gln Ile  
145 150 155 160

Ser Glu Asn Leu Phe Ser Asn Lys Val Leu Asn Ala Leu Lys Pro Glu  
165 170 175

Lys Asp Val Asp Gly Val Thr Asp Ile Asn Leu Gly Lys Leu Val Arg  
180 185 190

Gly Asp Ala His Glu Cys Phe Val Ser Pro Val Ala Lys Ala Val Ile  
195 200 205

Glu Leu Leu Glu Lys Ser Gly Val Asn Leu Asp Gly Lys Lys Ile Leu  
210 215 220

Val Val Gly Ala His Gly Ser Leu Glu Ala Ala Leu Gln Cys Leu Phe  
225 230 235 240

Gln Arg Lys Gly Ser Met Thr Met Ser Ile Gln Trp Lys Thr Arg Gln  
245 250 255

Leu Gln Ser Lys Leu His Glu Ala Asp Ile Val Val Leu Gly Ser Pro  
260 265 270

Lys Pro Glu Glu Ile Pro Leu Thr Trp Ile Gln Pro Gly Thr Thr Val  
275 280 285

Leu Asn Cys Ser His Asp Phe Leu Ser Gly Lys Val Gly Cys Gly Ser  
290 295 300

Pro Arg Ile His Phe Gly Gly Leu Ile Glu Glu Asp Asp Val Ile Leu  
305 310 315 320

Leu Ala Ala Ala Leu Arg Ile Gln Asn Met Val Ser Ser Gly Arg Arg  
325 330 335

Trp Leu Arg Glu Gln Gln His Arg Arg Trp Arg Leu His Cys Leu Lys  
340 345 350

Leu Gln Pro Leu Ser Pro Val Pro Ser Asp Ile Glu Ile Ser Arg Gly  
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Gln Thr Pro Lys Ala Val Asp Val Leu Ala Lys Glu Ile Gly Leu Leu  
370 375 380

Ala Asp Glu Ile Glu Ile Tyr G